

Table S3: Impact of aging on genes up-regulated by microbiota.

CG NUMBER	GENE SYMBOL	GENE category	GENE FUNCTION	Effect of microbiota on	
				young guts	old guts
				Canton S CR/AX	Canton S CR/AX
Young induced genes					
CG10901	osk	GENE EXPRESSION	regulation of mRNA stability	2.00	-1.17
CG4038	CG4038	GENE EXPRESSION	rRNA processing	1.30	1.18
CG13913	mwh	GUT STRUCTURE	actin binding	1.87	1.08
CG1558	Krn1	GUT STRUCTURE	chromosome segregation	1.30	1.01
CG13521	robo	GUT STRUCTURE	receptor activity	1.49	1.23
CG7629	AttD	IMMUNE RESPONSE	antimicrobial peptides	9.60	-1.12
CG32283	dro3	IMMUNE RESPONSE	antimicrobial peptides	1.72	1.28
CG16844	IM3	IMMUNE RESPONSE	DIMs	1.78	1.07
CG9976	Lectin-galC1	IMMUNE RESPONSE	lectin	1.41	1.14
CG31509	TotA	IMMUNE RESPONSE	Turandots	2.78	-1.05
CG14027	TotM	IMMUNE RESPONSE	Turandots	2.21	1.27
CG31508	TotC	IMMUNE RESPONSE	Turandots	1.53	-1.16
CG8577	PGRP-SC1a/b	IMMUNE RESPONSE	amidase activity	2.18	-1.40
CG14704	PGRP-LB	IMMUNE RESPONSE	amidase activity	1.39	1.28
CG9360	CG9360	METABOLISM/DIGESTION	carbohydrate digestion	1.84	-1.25
CG15695	CG15695	METABOLISM/DIGESTION	alkaline phosphatase	1.82	1.21
CG10559	CG10559	METABOLISM/DIGESTION	phosphorylation	1.39	-1.02
CG9259	CG9259	METABOLISM/DIGESTION	phosphorylation	1.32	1.00
CG7118	Jon66Ci	METABOLISM/DIGESTION	Jonah	2.12	1.04
CG6917	Est-6	METABOLISM/DIGESTION	peptidase	2.47	-1.04
CG30371	CG30371	METABOLISM/DIGESTION	serine protease	1.74	-1.07
CG11192	CG11192	METABOLISM/DIGESTION	serine protease	1.44	-1.02
CG12116	CG12116	METABOLISM/DIGESTION	folate metabolism	1.54	1.19
CG32041	Hsp22 /// Hsp67Bb	STRESS RESPONSE	HSP	2.74	-1.04
CG12242	GstD5	STRESS RESPONSE	glutathione transferase activity	1.42	-1.13
CG4381	GstD3	STRESS RESPONSE	glutathione transferase activity	1.30	-1.05
CG33109	CG33109	UNKNOWN	-	5.36	1.17
CG16826	CG16826	UNKNOWN	-	5.18	1.09
CG1678	CG1678	UNKNOWN	-	3.97	-1.07
CG12794	lcs	UNKNOWN	-	3.06	1.00
CG14292	CG14292	UNKNOWN	-	2.28	1.03
CG15068	CG15068	UNKNOWN	-	2.03	-1.07
CG16836	CG16836	UNKNOWN	-	1.62	-1.05
CG13309	CG13309	UNKNOWN	-	1.57	-1.14
CG11395	CG11395	UNKNOWN	-	1.46	-1.06
CG4716	CG4716	UNKNOWN	-	1.42	1.02
CG15067	CG15067	UNKNOWN	-	1.40	1.00
CG31436	CG31436	UNKNOWN	-	1.38	1.27
CG14688	CG14688	UNKNOWN	-	1.37	1.08
CG2233	CG2233	UNKNOWN	-	1.36	1.02
CG40271	CG40271	UNKNOWN	-	1.33	1.28
CG6188	CG6188	UNKNOWN	-	1.32	-1.17
CG6503	CG6503	UNKNOWN	-	1.32	-1.21
CG8317	CG8317	UNKNOWN	-	1.31	-1.34
CG10102	CG10102	UNKNOWN	binding	1.53	-1.12
CG14500	CG14500	UNKNOWN	binding	1.32	1.08
Young and old induced genes					
CG7670	WRNexo	GENE EXPRESSION	3'-5' exonuclease activity	1.69	1.61
CG6967	CG6967	GENE EXPRESSION	-	3.62	3.32
CG31421	Tak1	GENE EXPRESSION	MAP kinase kinase kinase activity	1.78	1.87
CG17950	HmgD	GENE EXPRESSION	-	1.34	1.49
CG15552	Sox100B	GENE EXPRESSION	DNA bending activity	1.50	1.76
X01472	Mef2	GENE EXPRESSION	RNA polymerase II transcription factor activity	1.40	1.44
CG8337	E(spl)malpa	GENE EXPRESSION	sequence-specific DNA binding	2.03	2.39
CG1070	Alh	GENE EXPRESSION	sequence-specific DNA binding transcription factor activity	1.61	2.84
CG12287	pdm2	GENE EXPRESSION	specific RNA polymerase II transcription factor activity	1.34	2.16
CG33983	obst-H	GUT STRUCTURE	chitin binding	1.31	2.64
CG3986	Chit4	GUT STRUCTURE	chitinase activity	1.38	2.14
CG31901	Mur29B	GUT STRUCTURE	chitin binding	1.70	1.78
CG32656	Muc11A	GUT STRUCTURE	mucin	2.17	2.01
CG7017	CG7017	GUT STRUCTURE	structural constituent of peritrophic membrane	1.39	2.03
CG13586	itp	GUT STRUCTURE	neuropeptide hormone activity	2.29	2.51
CG5730	AnniX	GUT STRUCTURE	calcium-dependent phospholipid binding	1.31	1.58
CG8095	scb	GUT STRUCTURE	cell adhesion molecule binding	1.36	2.11
CG1794	Mmp2	GUT STRUCTURE	matrix metalloproteinase	1.99	3.59
CG9579	AnnX	GUT STRUCTURE	actin binding	1.57	1.58
CG31363	Jupiter	GUT STRUCTURE	microtubule binding	1.61	1.77
CG7293	Klp68D	GUT STRUCTURE	motor activity	1.34	2.01
CG3401	betaTub60D	GUT STRUCTURE	structural constituent of cytoskeleton	2.72	3.12
CG12051	Act42A	GUT STRUCTURE	structural constituent of cytoskeleton	2.05	2.02

CG8091	Nc	GUT STRUCTURE	-	1.53	1.61
CG9193	mus209	GUT STRUCTURE	-	1.73	1.45
CG31453	pch2	GUT STRUCTURE	ATP binding	1.89	1.86
CG5940	CycA	GUT STRUCTURE	cyclin	2.02	1.96
CG11734	HERC2	GUT STRUCTURE	ubiquitin protein ligase	1.38	2.09
CG3897	blot	GUT STRUCTURE	neurotransmitter transporter activity	1.50	2.00
CG4700	Sema-2a	GUT STRUCTURE	protein binding	1.66	1.92
CG32279	dro2	IMMUNE RESPONSE	antimicrobial peptides	4.13	4.76
CG10146	AttA	IMMUNE RESPONSE	antimicrobial peptides	1.46	4.92
CG1385	Def	IMMUNE RESPONSE	antimicrobial peptides	1.40	4.49
CG4740	AttC	IMMUNE RESPONSE	antimicrobial peptides	1.36	1.42
CG18372	AttB	IMMUNE RESPONSE	antimicrobial peptides	1.55	2.15
CG10812	dro5	IMMUNE RESPONSE	antimicrobial peptides	1.37	2.10
CG15818	CG15818	IMMUNE RESPONSE	lectin	1.60	1.31
CG9120	LysX	IMMUNE RESPONSE	lysozyme	3.34	2.86
CG9116	LysP	IMMUNE RESPONSE	lysozyme	3.12	1.79
CG7496	PGRP-SD	IMMUNE RESPONSE	imd	2.71	2.31
CG16910	key	IMMUNE RESPONSE	imd	1.41	1.41
CG15678	pirk	IMMUNE RESPONSE	imd	2.06	1.76
CG6134	spz	IMMUNE RESPONSE	Toll cytokine	1.42	1.82
CG14934	mal_B1	METABOLISM/DIGESTION	maltase	1.98	1.58
CG32684	alpha-Man-I	METABOLISM/DIGESTION	mannosyl-oligosaccharide 1,2-alpha-mannosidase activity	1.48	1.72
CG10126	CG10126	METABOLISM/DIGESTION	calcium ion binding	1.48	1.43
CG15829	CG15829	METABOLISM/DIGESTION	fatty-acyl-CoA binding	2.72	3.62
CG17191	CG17191	METABOLISM/DIGESTION	triglyceride lipase activity	1.62	2.96
CG31148	CG31148	METABOLISM/DIGESTION	glucosylceramidase activity	1.45	1.83
CG7291	Npc2a	METABOLISM/DIGESTION	sterol binding	1.44	1.61
CG4860	CG4860	METABOLISM/DIGESTION	acyl-CoA dehydrogenase activity	1.44	1.38
CG10178	CG10178	METABOLISM/DIGESTION	glucuronosyltransferase activity	2.00	3.13
CG6869	FucTA	METABOLISM/DIGESTION	fucosyl transferase	1.52	2.29
CG4445	pgant3	METABOLISM/DIGESTION	polypeptide N-acetylgalactosaminyltransferase activity	1.68	2.35
CG18188	Damm	METABOLISM/DIGESTION	cysteine-type endopeptidase activity	1.31	1.75
CG5518	sda	METABOLISM/DIGESTION	aminopeptidase activity	1.50	2.00
CG3074	dmw	METABOLISM/DIGESTION	peptidase	1.62	3.56
CG4998	CG4998	METABOLISM/DIGESTION	serine-type endopeptidase activity	3.17	6.98
CG30090	CG30090	METABOLISM/DIGESTION	serine-type endopeptidase activity	2.24	1.84
CG8066	CG8066	METABOLISM/DIGESTION	homology cysteine-type endopeptidase inhibitor activity	1.33	1.63
CG1220	Kaz1-ORFB	METABOLISM/DIGESTION	serine-type endopeptidase inhibitor activity	1.51	1.83
CG31216	Naam	METABOLISM/DIGESTION	nicotinamidase activity	1.59	2.00
CG8975	RnrS	METABOLISM/DIGESTION	ribonucleoside-diphosphate reductase activity	1.68	1.40
CG5371	RnrL	METABOLISM/DIGESTION	ribonucleoside-diphosphate reductase activity	1.46	1.33
CG3181	Ts	METABOLISM/DIGESTION	thymidylate synthase activity	1.40	1.51
CG7816	CG7816	METABOLISM/DIGESTION	metal ion transmembrane transporter activity	1.60	1.65
CG31410	Npc2e	METABOLISM/DIGESTION	sterol transport	1.59	3.34
CG4799	Pen	METABOLISM/DIGESTION	protein transmembrane transporter activity	2.13	2.31
CG15009	ImpL2	SIGNALING	InR pathway	1.39	2.99
CG5963	upd3	SIGNALING	JAK-STAT pathway	1.61	2.22
CG15154	Socs36E	SIGNALING	JAK-STAT pathway	1.71	2.15
CG3619	DI	SIGNALING	Notch pathway	1.60	1.50
CG8346	HLLHm3	SIGNALING	Notch pathway	1.41	1.53
CG10580	fng	SIGNALING	Notch pathway	1.37	1.50
CG9670	fal	SIGNALING	other pathways	1.73	1.84
CG7103	Pvf1	SIGNALING	PVF pathway	2.15	2.50
CG2699	Pi3K21B	SIGNALING	transduction/modulation	1.79	2.13
CG13388	Akap200	SIGNALING	transduction/modulation	1.82	2.52
CG14031	Cyp4ac3	STRESS RESPONSE	electron carrier activity	1.31	1.34
CG4463	Hsp23	STRESS RESPONSE	HSP	15.29	4.54
CG18743	Hsp70Ab	STRESS RESPONSE	HSP	3.62	3.64
CG4183	Hsp26	STRESS RESPONSE	HSP	3.33	1.86
CG4466	Hsp27	STRESS RESPONSE	HSP	2.86	1.98
CG6489	Hsp70Bc	STRESS RESPONSE	HSP	2.13	2.00
CG6489	Hsp70Bc	STRESS RESPONSE	HSP	1.86	1.51
CG4421	GstD8	STRESS RESPONSE	glutathione transferase activity	1.42	1.50
CG42807	CG42807	UNKNOWN	-	22.70	7.02
CG15199	CG15199	UNKNOWN	-	5.00	1.91
CG32368	CG32368	UNKNOWN	-	4.73	3.49
CG12970	CG12970	UNKNOWN	-	4.68	5.84
CG6640	CG6640	UNKNOWN	-	3.79	2.95
CG4250	CG4250	UNKNOWN	-	3.32	8.46
CG8353	CG8353	UNKNOWN	-	3.13	2.22
CG13905	CG13905	UNKNOWN	-	3.07	3.75
CG14499	CG14499	UNKNOWN	-	3.02	1.66
CG4269	CG4269	UNKNOWN	-	2.71	1.32
CG14872	CG14872	UNKNOWN	binding	2.58	1.50
CG16995	CG16995	UNKNOWN	-	2.03	1.40
CG5630	CG5630	UNKNOWN	-	2.02	2.34

CG14696	CG14696	UNKNOWN	-	1.92	1.91
CG13488	CG13488	UNKNOWN	-	1.89	2.26
CG5118	CG5118	UNKNOWN	-	1.87	1.98
CG30154	CG30154	UNKNOWN	-	1.84	1.78
CG31344	CG31344	UNKNOWN	-	1.79	1.55
CG15065	CG15065	UNKNOWN	-	1.76	1.65
CG13190	cuff	UNKNOWN	-	1.63	2.31
CG31955	CG31955	UNKNOWN	binding	1.58	1.54
CG11885	CG11885	UNKNOWN	-	1.54	1.59
CG15083	CG15083	UNKNOWN	-	1.53	1.95
CG34236	CG34236	UNKNOWN	-	1.51	1.64
CG11671	CG11671	UNKNOWN	-	1.51	1.39
CG10943	CG10943	UNKNOWN	-	1.45	1.44
CG33468	CG33468	UNKNOWN	-	1.45	1.33
CG14872	CG14872	UNKNOWN	binding	1.44	1.50
CG18067	CG18067	UNKNOWN	-	1.40	1.31
CG15210	CG15210	UNKNOWN	-	1.39	1.81
CG11141	CG11141	UNKNOWN	-	1.38	1.54
CG5910	CG5910	UNKNOWN	-	1.38	1.42
CG13117	CG13117	UNKNOWN	-	1.36	2.78
CG14872	CG14872	UNKNOWN	binding	1.33	1.42
CG9411	CG9411	UNKNOWN	-	1.31	1.48
CG16762	CG16762	UNKNOWN	-	1.31	1.37
CG13177	CG13177	UNKNOWN	-	1.30	1.31
Old induced genes					
CG14906	CG14906	GENE EXPRESSION	homology DNA methylase	1.19	1.37
CG2914	Ets21C	GENE EXPRESSION	-	1.04	1.51
CG14029	vri	GENE EXPRESSION	negative regulation of transcription	1.09	1.50
CG4354	slbo	GENE EXPRESSION	RNA pol II regulation	1.27	3.85
CG6246	nub	GENE EXPRESSION	sequence-specific DNA binding transcription factor activity	-1.02	1.56
CG2054	Cht2	GUT STRUCTURE	chitinase activity	1.22	1.73
CG16963	Cry	GUT STRUCTURE	structural constituent of eye lens	1.29	1.51
CG5883	CG5883	GUT STRUCTURE	structural constituent of peritrophic membrane	1.14	1.82
CG7252	CG7252	GUT STRUCTURE	structural constituent of peritrophic membrane	-1.08	1.56
CG5897	CG5897	GUT STRUCTURE	structural constituent of peritrophic membrane	1.20	1.48
CG5803	Fas3	GUT STRUCTURE	-	1.19	1.79
CG5055	baz	GUT STRUCTURE	apico/basal polarity	1.06	1.70
CG1634	Nrg	GUT STRUCTURE	calcium ion binding	1.13	1.87
CG31004	CG31004	GUT STRUCTURE	cell-matrix adhesion	1.29	1.57
CG2534	cno	GUT STRUCTURE	actin binding	1.07	1.52
CG11949	cora	GUT STRUCTURE	cytoskeletal protein binding	1.24	2.04
CG8497	Rhp	GUT STRUCTURE	GTP-Rho binding	1.14	1.54
CG12946	Whamy	GUT STRUCTURE	GTPase binding	1.16	1.43
CG8566	unc-104	GUT STRUCTURE	microtubule binding	1.27	1.33
CG3178	Rrp1	GUT STRUCTURE	AP endonuclease, family	1.23	1.43
CG4978	Mcm7	GUT STRUCTURE	DNA helicase	1.26	1.47
CG6575	glec	IMMUNE RESPONSE	carbohydrate binding	1.01	2.12
CG5779	proPO-A1	IMMUNE RESPONSE	-	1.06	1.74
CG11331	Spn27A	IMMUNE RESPONSE	serine-type endopeptidase inhibitor activity	1.03	1.35
CG11992	Rel	IMMUNE RESPONSE	transcription factor	1.10	1.42
CG2086	drpr	IMMUNE RESPONSE	-	1.17	1.44
CG10383	CG10383	METABOLISM/DIGESTION	hydrolase activity, acting on ester bonds	-1.29	1.31
CG6271	CG6271	METABOLISM/DIGESTION	triglyceride lipase activity	1.02	1.30
CG10924	CG10924	METABOLISM/DIGESTION	phosphoenolpyruvate carboxykinase (GTP) activity	1.05	1.30
CG42329	CG42329	METABOLISM/DIGESTION	transferase activity, transferring acyl groups other than amino-acyl groups	1.02	2.31
CG42329	CG42329	METABOLISM/DIGESTION	transferase activity, transferring acyl groups other than amino-acyl groups	-1.01	1.98
CG3881	GlcAT-S	METABOLISM/DIGESTION	galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase activity	1.11	1.40
CG10000	CG10000	METABOLISM/DIGESTION	polypeptide N-acetylgalactosaminyltransferase activity	1.22	1.82
CG6357	CG6357	METABOLISM/DIGESTION	cysteine-type endopeptidase activity	-1.09	1.38
CG31313	CG31313	METABOLISM/DIGESTION	cysteine-type endopeptidase inhibitor activity	1.26	1.71
CG14526	CG14526	METABOLISM/DIGESTION	metalloendopeptidase activity	1.26	1.50
CG10663	CG10663	METABOLISM/DIGESTION	Peptidase S1/S6	1.20	1.64
CG6639	CG6639	METABOLISM/DIGESTION	serine-type endopeptidase activity	1.22	1.65
CG6330	CG6330	METABOLISM/DIGESTION	uridine phosphorylase activity	1.29	1.50
CG1358	CG1358	METABOLISM/DIGESTION	-	1.07	1.38
CG6125	CG6125	METABOLISM/DIGESTION	high affinity sulfate transmembrane transporter activity	1.07	1.52
CG13893	CG13893	METABOLISM/DIGESTION	transporter activity	1.10	1.33
CG17077	pnt	SIGNALING	EGFR pathway	1.18	1.73
CG10491	vn	SIGNALING	EGFR pathway	1.18	1.68
CG1004	rho	SIGNALING	EGFR pathway	1.12	2.50
CG4608	bnl	SIGNALING	FGF pathway	1.02	1.48
CG4637	hh	SIGNALING	hh pathway	1.09	1.90
CG18402	lnR	SIGNALING	lnR pathway	1.11	2.46
CG15509	kay	SIGNALING	JNK pathway	1.21	1.67
CG3973	pigs	SIGNALING	Notch pathway	1.06	1.74
CG11988	neur	SIGNALING	Notch pathway	1.07	1.57

CG14080	Mkp3	SIGNALING	other pathways	-1.02	2.16
CG5212	Pli	SIGNALING	other pathways	1.06	1.33
CG31794	Pax	SIGNALING	other pathways	1.17	1.73
CG2849	Rala	SIGNALING	other pathways	1.16	1.48
CG31811	cenG1A	SIGNALING	transduction/modulation	-1.08	1.65
CG31543	Hph	STRESS RESPONSE	peptidyl-proline 4-dioxygenase activity	-1.05	1.46
CG33111	CG33111	STRESS RESPONSE	oxidoreductase activity	1.15	1.47
CG32556	CG32556	UNKNOWN	-	1.09	2.41
CG30082	CG30082	UNKNOWN	-	1.27	2.10
CG2679	gol	UNKNOWN	-	1.28	1.99
CG11658	CG11658	UNKNOWN	-	1.10	1.80
CG8678	CG8678	UNKNOWN	-	1.27	1.76
CG6490	CG6490	UNKNOWN	-	1.10	1.75
CG5953	CG5953	UNKNOWN	-	-1.11	1.74
CG18635	CG18635	UNKNOWN	-	1.29	1.72
CG10106	Tsp42Ee	UNKNOWN	-	1.23	1.72
CG42388	CG42388	UNKNOWN	-	1.09	1.70
CG13506	CG13506	UNKNOWN	-	1.12	1.65
CG13598	sba	UNKNOWN	-	1.24	1.64
CG42388	CG42388	UNKNOWN	-	1.20	1.63
CG3703	CG3703	UNKNOWN	-	1.18	1.61
CG8965	CG8965	UNKNOWN	-	1.28	1.59
CG17264	CG17264	UNKNOWN	-	1.15	1.58
CG15893	CG15893	UNKNOWN	-	1.21	1.55
CG42565	CG42565	UNKNOWN	-	1.23	1.53
CG34232	CG34232	UNKNOWN	-	-1.01	1.49
CG8398	CG8398	UNKNOWN	-	1.29	1.48
CG5123	W	UNKNOWN	-	-1.27	1.48
CG30015	CG30015	UNKNOWN	-	-1.00	1.42
CG33469	CG33469	UNKNOWN	-	1.25	1.40
CG33146	Mctp	UNKNOWN	-	1.21	1.38
CG14302	CG14302	UNKNOWN	-	1.06	1.38
CG1347	CG1347	UNKNOWN	-	-1.00	1.38
CG13511	CG13511	UNKNOWN	-	1.00	1.37
CG11093	CG11093	UNKNOWN	-	-1.02	1.37
CG42394	CG42394	UNKNOWN	-	1.12	1.36
CG13482	CG13482	UNKNOWN	-	1.12	1.36
CG5073	CG5073	UNKNOWN	-	1.06	1.35
CG13877	CG13877	UNKNOWN	-	1.21	1.34
CG9989	CG9989	UNKNOWN	-	-1.36	1.34
CG4300	CG4300	UNKNOWN	-	1.28	1.33
CG11242	CG11242	UNKNOWN	-	1.26	1.33
CG32373	CG32373	UNKNOWN	-	1.05	1.30
CG4393	CG4393	UNKNOWN	-	1.01	1.30
CG13510	CG13510	UNKNOWN	-	1.00	1.30
CG6792	CG6792	UNKNOWN	-	-1.06	1.30

<-1.3
 <-2.0
 <-4.0
 >1.3
 >2
 >4
 >10